

Interference - EAST

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	2	"2002156262".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:18
S2	2	"20020156262".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:18
S3	5	"2004043465".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:18
S4	2	"20040043465".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:19
S5	1	"20040082049".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:20
S6	2	"20040086996".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/11/08 12:08
S7	2	"200037655".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:21
S8	2	"200037655".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:22
S9	28	leung.in. and Ipaat	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:24
S10	2	"2000175684".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:28
S11	2	"20020156262".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:53
S12	2	"20030073174".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/11/03 14:53

S13	2	"6300487".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/11/08 12:07
S14	2	"6670143".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/28 16:01
S15	2	"6670143".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/11/08 12:05
S16	2	"6136964".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/11/08 12:07
S17	5003	leung.in. or adourel.in. or hollenback. in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/11/08 12:09
S18	9	S17 and (lysophosphatidic and (SEQ adj ID).clm.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/11/08 12:09

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 17:58:26 ; Search time 3812 Seconds
(without alignments)
3991.327 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140055_12066/app_query.fasta_1
.455
-DB=GenEmbl -QFMT=fastap -SUFFIX=na.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462@CGN_1_1_5600@runat_14062005_140055_12066 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

 13: gb_un:*

 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1682	100.0	1314	6	CQ731857	CQ731857 Sequence
2	1682	100.0	1333	6	E39269	E39269 Gene encodi
3	1682	100.0	1333	9	AB040138	AB040138 Homo sapi
4	1682	100.0	1523	6	BD265489	BD265489 Mammalian
5	1682	100.0	1523	6	AR370495	AR370495 Sequence
6	1682	100.0	1523	6	AR442694	AR442694 Sequence
7	1682	100.0	1523	9	AF156775	AF156775 Homo sapi
8	1682	100.0	1577	9	BC011971	BC011971 Homo sapi
9	1682	100.0	1660	6	BD265488	BD265488 Mammalian
10	1682	100.0	1660	6	AR370494	AR370494 Sequence
11	1682	100.0	1660	6	AR442693	AR442693 Sequence
12	1682	100.0	1660	9	AF156774	AF156774 Homo sapi
13	1682	100.0	1960	6	AX317982	AX317982 Sequence
14	1682	100.0	2377	9	BC063552	BC063552 Homo sapi
15	1682	100.0	2397	9	BC040603	BC040603 Homo sapi
16	1678	99.8	1128	6	AX239832	AX239832 Sequence
17	1678	99.8	1832	6	AX239824	AX239824 Sequence
18	1662	98.8	3955	6	CQ842883	CQ842883 Sequence
19	1662	98.8	3955	9	AK125804	AK125804 Homo sapi
20	1598	95.0	1153	10	AY167588	AY167588 Mus muscu
21	1598	95.0	3378	10	BC058519	BC058519 Mus muscu
22	1598	95.0	3379	10	BC052382	BC052382 Mus muscu
23	1593.5	94.7	3060	6	AX376270	AX376270 Sequence
24	1593.5	94.7	3060	6	AX697228	AX697228 Sequence
25	1593.5	94.7	3060	9	AY358704	AY358704 Homo sapi
26	1561	92.8	5633	6	BD183432	BD183432 Novel gen
27	1538	91.4	1769	6	AR339350	AR339350 Sequence
28	1432	85.1	4208	5	BC081052	BC081052 Xenopus l
29	1428	84.9	2728	5	BC081323	BC081323 Xenopus t
30	1420	84.4	3509	5	BC043776	BC043776 Xenopus l
31	1387	82.5	3878	6	AX211367	AX211367 Sequence
32	1286.5	76.5	2447	5	BC049474	BC049474 Danio rer
33	1145	68.1	1245	5	BX929790	BX929790 Gallus ga
34	1138	67.7	1540	5	BC071000	BC071000 Xenopus l
35	1094	65.0	1137	6	AX119047	AX119047 Sequence
36	1094	65.0	1721	9	BC020209	BC020209 Homo sapi
37	1094	65.0	1771	6	AX135548	AX135548 Sequence
38	1094	65.0	1774	6	BD265490	BD265490 Mammalian
39	1094	65.0	1774	6	AR370496	AR370496 Sequence
40	1094	65.0	1774	6	AR442695	AR442695 Sequence
41	1094	65.0	1774	9	AF156776	AF156776 Homo sapi
42	1094	65.0	1781	6	AR252488	AR252488 Sequence
43	1094	65.0	1781	6	AR528661	AR528661 Sequence
44	1094	65.0	1781	6	AX056649	AX056649 Sequence

45 1094 65.0 1781 6 AX403268

AX403268 Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 17:41:30 ; Search time 517 Seconds
(without alignments)
3595.355 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140055_12057/app_query.fasta_1
.455
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=na.rng -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462@CGN_1_1_708@runat_14062005_140055_12057 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:

12: geneseqn2004as:
 13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1682	100.0	1333	3	AAA71493	Aaa71493 Human lys
2	1682	100.0	1523	3	AAA51069	Aaa51069 Human LPA
3	1682	100.0	1523	6	AAD24424	Aad24424 Human LPA
4	1682	100.0	1523	9	ABX16125	Abx16125 Human cDN
5	1682	100.0	1523	12	ADJ93798	Adj93798 Human lys
6	1682	100.0	1523	12	ADN49482	Adn49482 Human lys
7	1682	100.0	1523	12	ADO04621	Ado04621 Human lys
8	1682	100.0	1629	6	ABL55080	Abl55080 Human cDN
9	1682	100.0	1646	12	ADQ85949	Adq85949 Human tum
10	1682	100.0	1660	3	AAA51068	Aaa51068 Human LPA
11	1682	100.0	1660	6	AAD24423	Aad24423 Human LPA
12	1682	100.0	1660	9	ABX16124	Abx16124 Human cDN
13	1682	100.0	1660	12	ADJ93796	Adj93796 Human lys
14	1682	100.0	1660	12	ADN49480	Adn49480 Human lys
15	1682	100.0	1660	12	ADO04619	Ado04619 Human lys
16	1682	100.0	1660	13	ACN40851	Acn40851 Tumour-as
17	1682	100.0	1960	6	AAD24014	Aad24014 Human dru
18	1678	99.8	1832	5	AAH75152	Aah75152 Nucleotid
19	1678	99.8	1832	12	ADQ15077	Adq15077 Human can
20	1678	99.8	1832	13	ADR40140	Adr40140 Human lys
21	1662	98.8	3955	12	ADQ64369	Adq64369 Novel hum
22	1593.5	94.7	3059	4	AAS46093	Aas46093 Human DNA
23	1593.5	94.7	3060	3	AAA37104	Aaa37104 Human PRO
24	1593.5	94.7	3060	4	AAF54413	Aaf54413 Primer #8
25	1593.5	94.7	3060	8	ACA89543	Aca89543 cDNA enco
26	1593.5	94.7	3060	8	ACA73553	Aca73553 Human sec
27	1593.5	94.7	3060	8	ACA05868	Aca05868 Human sec
28	1593.5	94.7	3060	8	ACA66702	Aca66702 cDNA enco
29	1593.5	94.7	3060	8	ACF20277	Acf20277 Human sec
30	1593.5	94.7	3060	8	ACF19663	Acf19663 Human sec
31	1593.5	94.7	3060	8	ACD21951	Acd21951 Human sec
32	1593.5	94.7	3060	8	ACF13116	Acf13116 Human sec
33	1593.5	94.7	3060	8	ACD25219	Acd25219 Human sec
34	1593.5	94.7	3060	8	ACF00268	Acf00268 Human sec
35	1593.5	94.7	3060	8	ACA72325	Aca72325 Novel hum
36	1593.5	94.7	3060	8	ACD04849	Acd04849 Novel hum
37	1593.5	94.7	3060	8	ACD18310	Acd18310 Human sec
38	1593.5	94.7	3060	8	ACD08317	Acd08317 Human sec
39	1593.5	94.7	3060	8	ACA88751	Aca88751 Novel hum
40	1593.5	94.7	3060	8	ACA70193	Aca70193 Human sec
41	1593.5	94.7	3060	8	ACD12415	Acd12415 Novel hum
42	1593.5	94.7	3060	8	ACC74330	Acc74330 Human sec
43	1593.5	94.7	3060	8	ACD15958	Acd15958 Human sec
44	1593.5	94.7	3060	8	ACD25526	Acd25526 Novel hum
45	1593.5	94.7	3060	8	ACD18003	Acd18003 Human sec

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 18:06:16 ; Search time 188 Seconds
(without alignments)
2732.930 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140056_12095/app_query.fasta_1
.455
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=na.rni -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462@CGN_1_1_105@runat_14062005_140056_12095 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	1682	100.0	1523	3	US-09-215-252-14	Sequence 14, Appl
	2	1682	100.0	1523	4	US-09-970-989A-14	Sequence 14, Appl
	3	1682	100.0	1660	3	US-09-215-252-12	Sequence 12, Appl
	4	1682	100.0	1660	4	US-09-970-989A-12	Sequence 12, Appl
	5	1538	91.4	1769	4	US-09-620-312D-841	Sequence 841, App
	6	1094	65.0	1774	3	US-09-215-252-16	Sequence 16, Appl
	7	1094	65.0	1774	4	US-09-970-989A-16	Sequence 16, Appl
	8	513	30.5	1515	4	US-08-818-581B-3	Sequence 3, Appli
	9	496.5	29.5	1514	2	US-08-454-267-1	Sequence 1, Appli
	10	496.5	29.5	1514	2	US-08-941-319-1	Sequence 1, Appli
	11	496.5	29.5	1514	3	US-09-035-098-1	Sequence 1, Appli
	12	247	14.7	271	4	US-09-513-999C-10074	Sequence 10074, A
	13	231	13.7	1763	4	US-09-620-312D-637	Sequence 637, App
	14	228	13.6	5227	2	US-08-996-306-3	Sequence 3, Appli
	15	228	13.6	5245	3	US-09-338-907-3	Sequence 3, Appli
	16	228	13.6	5245	3	US-09-218-207-3	Sequence 3, Appli
	17	228	13.6	5290	3	US-09-338-907-119	Sequence 119, App
	18	228	13.6	5290	3	US-09-218-207-119	Sequence 119, App
	19	222	13.2	5250	3	US-09-338-907-69	Sequence 69, Appl
	20	222	13.2	5250	3	US-09-218-207-69	Sequence 69, Appl
	21	219.5	13.0	1409	3	US-09-338-907-72	Sequence 72, Appl
	22	219.5	13.0	1409	3	US-09-338-907-184	Sequence 184, App
	23	219.5	13.0	1409	3	US-09-218-207-72	Sequence 72, Appl
	24	219.5	13.0	1409	3	US-09-218-207-184	Sequence 184, App
	25	195.5	11.6	5148	3	US-09-338-907-112	Sequence 112, App
	26	195.5	11.6	5148	3	US-09-218-207-112	Sequence 112, App
	27	191.5	11.4	5326	3	US-09-338-907-124	Sequence 124, App
	28	191.5	11.4	5326	3	US-09-218-207-124	Sequence 124, App
	29	186	11.1	5234	3	US-09-338-907-113	Sequence 113, App
	30	186	11.1	5234	3	US-09-218-207-113	Sequence 113, App
	31	177	10.5	5044	3	US-09-338-907-115	Sequence 115, App
	32	177	10.5	5044	3	US-09-218-207-115	Sequence 115, App
	33	174.5	10.4	4958	3	US-09-338-907-116	Sequence 116, App
	34	174.5	10.4	4958	3	US-09-218-207-116	Sequence 116, App
	35	173	10.3	775	4	US-09-220-132-191	Sequence 191, App
	36	170	10.1	5020	3	US-09-338-907-120	Sequence 120, App
	37	170	10.1	5020	3	US-09-218-207-120	Sequence 120, App
c	38	165	9.8	1629	4	US-09-252-991A-13111	Sequence 13111, A
	39	161.5	9.6	960	4	US-09-540-236-1906	Sequence 1906, Ap
c	40	161.5	9.6	31940	4	US-09-596-002-13	Sequence 13, Appl
	41	161	9.6	969	4	US-09-252-991A-12688	Sequence 12688, A
	42	161	9.6	1041	4	US-09-252-991A-12831	Sequence 12831, A
	43	152	9.0	1095	4	US-09-252-991A-5981	Sequence 5981, Ap
	44	152	9.0	1200	4	US-09-252-991A-5964	Sequence 5964, Ap
c	45	152	9.0	1515	4	US-09-252-991A-5909	Sequence 5909, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 19:42:57 ; Search time 571 Seconds
(without alignments)
3408.940 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140058_12181/app_query.fasta_1
.455
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=na.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10667462@CGN_1_1_723@runat_14062005_140058_12181
-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1682	100.0	1523	9	US-09-970-989-14	Sequence 14, Appl
2	1682	100.0	1523	18	US-10-667-494-14	Sequence 14, Appl
3	1682	100.0	1523	18	US-10-667-462-14	Sequence 14, Appl
4	1682	100.0	1523	18	US-10-667-464-14	Sequence 14, Appl
5	1682	100.0	1660	9	US-09-970-989-12	Sequence 12, Appl
6	1682	100.0	1660	18	US-10-667-494-12	Sequence 12, Appl
7	1682	100.0	1660	18	US-10-667-462-12	Sequence 12, Appl
8	1682	100.0	1660	18	US-10-667-464-12	Sequence 12, Appl
9	1682	100.0	1960	17	US-10-296-606-22	Sequence 22, Appl
10	1678	99.8	1128	9	US-09-798-029-13	Sequence 13, Appl
11	1678	99.8	1832	9	US-09-798-029-5	Sequence 5, Appl
12	1678	99.8	1832	20	US-10-737-450-35	Sequence 35, Appl
13	1678	99.8	1832	21	US-10-772-636-21	Sequence 21, Appl
14	1593.5	94.7	3060	10	US-09-946-374-296	Sequence 296, App
15	1593.5	94.7	3060	13	US-10-052-586-337	Sequence 337, App
16	1593.5	94.7	3060	14	US-10-174-590-337	Sequence 337, App
17	1593.5	94.7	3060	14	US-10-176-758-337	Sequence 337, App
18	1593.5	94.7	3060	14	US-10-175-737-337	Sequence 337, App
19	1593.5	94.7	3060	14	US-10-174-581-337	Sequence 337, App
20	1593.5	94.7	3060	14	US-10-176-483-337	Sequence 337, App
21	1593.5	94.7	3060	14	US-10-176-749-337	Sequence 337, App
22	1593.5	94.7	3060	14	US-10-176-914-337	Sequence 337, App
23	1593.5	94.7	3060	14	US-10-176-915-337	Sequence 337, App
24	1593.5	94.7	3060	14	US-10-173-706-337	Sequence 337, App
25	1593.5	94.7	3060	14	US-10-175-738-337	Sequence 337, App
26	1593.5	94.7	3060	14	US-10-175-752-337	Sequence 337, App
27	1593.5	94.7	3060	14	US-10-176-482-337	Sequence 337, App
28	1593.5	94.7	3060	14	US-10-176-757-337	Sequence 337, App
29	1593.5	94.7	3060	14	US-10-176-913-337	Sequence 337, App
30	1593.5	94.7	3060	14	US-10-180-552-337	Sequence 337, App
31	1593.5	94.7	3060	14	US-10-180-557-337	Sequence 337, App
32	1593.5	94.7	3060	14	US-10-173-700-337	Sequence 337, App

33	1593.5	94.7	3060	14	US-10-174-572-337	Sequence 337, App
34	1593.5	94.7	3060	14	US-10-174-579-337	Sequence 337, App
35	1593.5	94.7	3060	14	US-10-174-582-337	Sequence 337, App
36	1593.5	94.7	3060	14	US-10-174-588-337	Sequence 337, App
37	1593.5	94.7	3060	14	US-10-175-739-337	Sequence 337, App
38	1593.5	94.7	3060	14	US-10-175-740-337	Sequence 337, App
39	1593.5	94.7	3060	14	US-10-175-743-337	Sequence 337, App
40	1593.5	94.7	3060	14	US-10-176-488-337	Sequence 337, App
41	1593.5	94.7	3060	14	US-10-176-492-337	Sequence 337, App
42	1593.5	94.7	3060	14	US-10-176-747-337	Sequence 337, App
43	1593.5	94.7	3060	14	US-10-176-750-337	Sequence 337, App
44	1593.5	94.7	3060	14	US-10-176-985-337	Sequence 337, App
45	1593.5	94.7	3060	14	US-10-176-987-337	Sequence 337, App

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 18:05:07 ; Search time 3118 Seconds
(without alignments)
3833.284 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-

Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140056_12079/app_query.fasta_1
.455

-DB=EST -QFMT=fastap -SUFFIX=na.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10667462@CGN_1_1_5180@runat_14062005_140056_12079 -NCPU=6 -ICPU=3

-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
	1	1619	96.3	5079	3	HSM804230
	2	1598	95.0	1319	3	AK015906
	3	1598	95.0	1415	3	AK076414
	4	1598	95.0	3022	3	BC033444
	5	1598	95.0	3439	3	AK075715
	6	1589	94.5	3240	3	AK030607
	7	1513	90.0	1558	3	AK008965
c	8	1415.5	84.2	986	4	BI408757
	9	1388	82.5	1063	4	BM459459
	10	1374	81.7	1131	9	AY419544
	11	1303	77.5	1131	9	AY419546
	12	1279	76.0	797	7	CO886199
	13	1260	74.9	808	5	BU126102
	14	1258.5	74.8	985	5	BQ072125
	15	1245	74.0	735	6	CD350550
c	16	1172.5	69.7	881	4	BI100258
	17	1165.5	69.3	1183	6	CD505010
	18	1141	67.8	1131	9	AY419545
c	19	1138	67.7	675	4	BM675712
	20	1137	67.6	669	7	CO432267
	21	1120	66.6	656	2	AW411232
	22	1113	66.2	827	6	CD303142
	23	1105.5	65.7	1024	4	BG424827
	24	1094	65.0	1137	9	AY404676
	25	1094	65.0	1690	3	CR609642
	26	1094	65.0	1737	3	CR615061
	27	1094	65.0	1756	3	CR623504
	28	1094	65.0	1781	3	CR615644
	29	1094	65.0	1786	3	CR612654
	30	1090	64.8	703	4	BG995044
	31	1085	64.5	971	5	BX401713
	32	1085	64.5	1912	3	AK005139
	33	1085	64.5	2084	3	BC031179
	34	1083	64.4	1137	9	AY404678
	35	1080	64.2	976	5	BU840364
	36	1071	63.7	648	2	AW410448
	37	1070	63.6	637	7	CF744159
	38	1070	63.6	1137	9	AY404677
c	39	1063	63.2	871	7	CK773096
	40	1060	63.0	780	5	BU421664
	41	1058	62.9	622	2	BE298682
	42	1051.5	62.5	896	4	BG541849
	43	1048	62.3	919	5	BX325280
	44	1045	62.1	871	7	CR565259
	45	1035.5	61.6	1144	5	BQ049014

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OM protein - protein search, using sw model

Run on: June 14, 2005, 16:00:31 ; Search time 119 Seconds
(without alignments)
1020.527 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1682	100.0	314	3	AAY96591	Aay96591 Human lys
2	1682	100.0	314	5	AAE15295	Aae15295 Human LPA
3	1682	100.0	314	6	ABG74254	Abg74254 Human LPA
4	1682	100.0	314	8	ADJ93799	Adj93799 Human lys
5	1682	100.0	314	8	ADN49483	Adn49483 Human lys
6	1682	100.0	314	8	ADO04622	Ado04622 Human lys
7	1682	100.0	376	3	AAY96590	Aay96590 Human lys
8	1682	100.0	376	3	AAB10460	Aab10460 Human lys
9	1682	100.0	376	5	AAE15294	Aae15294 Human LPA
10	1682	100.0	376	5	ABG64898	Abg64898 Human alb

11	1682	100.0	376	5	ABB77011	Abb77011 Human pro
12	1682	100.0	376	5	AAE14446	Aae14446 Human dru
13	1682	100.0	376	6	ABG74253	Abg74253 Human LPA
14	1682	100.0	376	8	ADL78165	Adl78165 Albumin f
15	1682	100.0	376	8	ADJ93797	Adj93797 Human lys
16	1682	100.0	376	8	ADN49481	Adn49481 Human lys
17	1682	100.0	376	8	ADO04620	Ado04620 Human lys
18	1682	100.0	376	8	ABM82301	Abm82301 Tumour-as
19	1678	99.8	376	4	AAG67124	Aag67124 Amino aci
20	1678	99.8	376	8	ADQ15078	Adq15078 Human can
21	1678	99.8	376	8	ADR40141	Adr40141 Human lys
22	1662	98.8	392	8	ADQ66557	Adq66557 Novel hum
23	1585.5	94.3	368	3	AAY99422	Aay99422 Human PRO
24	1585.5	94.3	368	4	AAB66171	Aab66171 Protein o
25	1585.5	94.3	368	4	AAU29192	Aau29192 Human PRO
26	1585.5	94.3	368	6	ABU58568	Abu58568 Human PRO
27	1585.5	94.3	368	6	ABU88116	Abu88116 Novel hum
28	1585.5	94.3	368	6	ABU84431	Abu84431 Human sec
29	1585.5	94.3	368	6	ABR66305	Abr66305 Human sec
30	1585.5	94.3	368	6	ABR65695	Abr65695 Human sec
31	1585.5	94.3	368	6	ABU99635	Abu99635 Human sec
32	1585.5	94.3	368	6	ABU82874	Abu82874 Human PRO
33	1585.5	94.3	368	6	ABU89995	Abu89995 Novel hum
34	1585.5	94.3	368	6	ABR68244	Abr68244 Human sec
35	1585.5	94.3	368	6	ABU96297	Abu96297 Novel hum
36	1585.5	94.3	368	6	ABU92728	Abu92728 Human sec
37	1585.5	94.3	368	6	ABO08805	Abo08805 Human sec
38	1585.5	94.3	368	6	ABO02857	Abo02857 Human sec
39	1585.5	94.3	368	6	ABR75011	Abr75011 Human sec
40	1585.5	94.3	368	6	ABR94773	Abr94773 Human sec
41	1585.5	94.3	368	6	ABU85746	Abu85746 Human PRO
42	1585.5	94.3	368	6	ABU98906	Abu98906 Novel hum
43	1585.5	94.3	368	6	ABU98121	Abu98121 Novel hum
44	1585.5	94.3	368	6	ABU91827	Abu91827 Novel hum
45	1585.5	94.3	368	6	ABU89520	Abu89520 Human PRO

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OM protein - protein search, using sw model

Run on: June 14, 2005, 17:25:00 ; Search time 45 Seconds
(without alignments)
520.885 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1682	100.0	314	3	US-09-215-252-15	Sequence 15, Appl
2	1682	100.0	314	4	US-09-970-989A-15	Sequence 15, Appl
3	1682	100.0	376	3	US-09-215-252-13	Sequence 13, Appl
4	1682	100.0	376	4	US-09-970-989A-13	Sequence 13, Appl
5	1094	65.0	378	3	US-09-215-252-17	Sequence 17, Appl
6	1094	65.0	378	4	US-09-970-989A-17	Sequence 17, Appl
7	513	30.5	377	4	US-08-818-581B-4	Sequence 4, Appl
8	496.5	29.5	374	2	US-08-454-267-2	Sequence 2, Appl
9	496.5	29.5	374	2	US-08-454-267-6	Sequence 6, Appl
10	496.5	29.5	374	2	US-08-941-319-2	Sequence 2, Appl
11	496.5	29.5	374	2	US-08-941-319-6	Sequence 6, Appl
12	496.5	29.5	374	3	US-09-035-098-2	Sequence 2, Appl

13	496.5	29.5	374	3	US-09-035-098-6	Sequence 6, Appli
14	496.5	29.5	374	3	US-09-215-252-5	Sequence 5, Appli
15	496.5	29.5	374	4	US-09-970-989A-5	Sequence 5, Appli
16	488.5	29.0	375	4	US-08-818-581B-5	Sequence 5, Appli
17	389.5	23.2	295	2	US-08-454-267-7	Sequence 7, Appli
18	389.5	23.2	295	2	US-08-941-319-7	Sequence 7, Appli
19	389.5	23.2	295	3	US-09-035-098-7	Sequence 7, Appli
20	389.5	23.2	311	4	US-08-818-581B-6	Sequence 6, Appli
21	228	13.6	353	2	US-08-996-306-4	Sequence 4, Appli
22	228	13.6	353	3	US-09-338-907-4	Sequence 4, Appli
23	228	13.6	353	3	US-09-218-207-4	Sequence 4, Appli
24	228	13.6	364	2	US-08-996-306-5	Sequence 5, Appli
25	228	13.6	364	3	US-09-338-907-5	Sequence 5, Appli
26	228	13.6	364	3	US-09-218-207-5	Sequence 5, Appli
27	219.5	13.0	354	3	US-09-338-907-74	Sequence 74, Appl
28	219.5	13.0	354	3	US-09-218-207-74	Sequence 74, Appl
29	177	10.5	291	3	US-09-338-907-127	Sequence 127, App
30	177	10.5	291	3	US-09-218-207-127	Sequence 127, App
31	175.5	10.4	228	3	US-09-338-907-70	Sequence 70, Appl
32	175.5	10.4	228	3	US-09-218-207-70	Sequence 70, Appl
33	174.5	10.4	261	3	US-09-338-907-128	Sequence 128, App
34	174.5	10.4	261	3	US-09-218-207-128	Sequence 128, App
35	161.5	9.6	319	4	US-09-540-236-3826	Sequence 3826, Ap
36	161	9.6	346	4	US-09-252-991A-29402	Sequence 29402, A
37	152	9.0	364	4	US-09-252-991A-22552	Sequence 22552, A
38	148.5	8.8	321	4	US-09-328-352-5730	Sequence 5730, Ap
39	135	8.0	320	4	US-09-489-039A-10418	Sequence 10418, A
40	133	7.9	23	3	US-09-215-252-29	Sequence 29, Appl
41	133	7.9	23	4	US-09-970-989A-29	Sequence 29, Appl
42	130	7.7	315	3	US-09-338-907-134	Sequence 134, App
43	130	7.7	315	3	US-09-218-207-134	Sequence 134, App
44	122.5	7.3	300	3	US-09-338-907-135	Sequence 135, App
45	122.5	7.3	300	3	US-09-218-207-135	Sequence 135, App

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OM protein - protein search, using sw model

Run on: June 14, 2005, 17:39:11 ; Search time 1394 Seconds
(without alignments)
86.346 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
1	1682	100.0	314	9	US	09-970-989-15	Sequence 15, Appl
2	1682	100.0	314	15	US	10-667-494-15	Sequence 15, Appl
3	1682	100.0	314	15	US	10-667-462-15	Sequence 15, Appl
4	1682	100.0	314	15	US	10-667-464-15	Sequence 15, Appl
5	1682	100.0	376	9	US	09-970-989-13	Sequence 13, Appl
6	1682	100.0	376	11	US	09-833-245-1647	Sequence 1647, Ap
7	1682	100.0	376	15	US	10-296-606-9	Sequence 9, Appl
8	1682	100.0	376	15	US	10-667-494-13	Sequence 13, Appl
9	1682	100.0	376	15	US	10-667-462-13	Sequence 13, Appl
10	1682	100.0	376	15	US	10-667-464-13	Sequence 13, Appl
11	1678	99.8	376	9	US	09-798-029-6	Sequence 6, Appl
12	1678	99.8	376	16	US	10-737-450-36	Sequence 36, Appl
13	1678	99.8	376	17	US	10-772-636-22	Sequence 22, Appl
14	1585.5	94.3	368	10	US	09-946-374-297	Sequence 297, App
15	1585.5	94.3	368	13	US	10-052-586-338	Sequence 338, App
16	1585.5	94.3	368	14	US	10-174-590-338	Sequence 338, App
17	1585.5	94.3	368	14	US	10-176-758-338	Sequence 338, App
18	1585.5	94.3	368	14	US	10-175-737-338	Sequence 338, App
19	1585.5	94.3	368	14	US	10-174-581-338	Sequence 338, App
20	1585.5	94.3	368	14	US	10-176-483-338	Sequence 338, App
21	1585.5	94.3	368	14	US	10-176-749-338	Sequence 338, App
22	1585.5	94.3	368	14	US	10-176-914-338	Sequence 338, App
23	1585.5	94.3	368	14	US	10-176-915-338	Sequence 338, App
24	1585.5	94.3	368	14	US	10-173-706-338	Sequence 338, App
25	1585.5	94.3	368	14	US	10-175-738-338	Sequence 338, App
26	1585.5	94.3	368	14	US	10-175-752-338	Sequence 338, App
27	1585.5	94.3	368	14	US	10-176-482-338	Sequence 338, App
28	1585.5	94.3	368	14	US	10-176-757-338	Sequence 338, App
29	1585.5	94.3	368	14	US	10-176-913-338	Sequence 338, App
30	1585.5	94.3	368	14	US	10-180-552-338	Sequence 338, App
31	1585.5	94.3	368	14	US	10-180-557-338	Sequence 338, App
32	1585.5	94.3	368	14	US	10-173-700-338	Sequence 338, App
33	1585.5	94.3	368	14	US	10-174-572-338	Sequence 338, App
34	1585.5	94.3	368	14	US	10-174-579-338	Sequence 338, App
35	1585.5	94.3	368	14	US	10-174-582-338	Sequence 338, App
36	1585.5	94.3	368	14	US	10-174-588-338	Sequence 338, App
37	1585.5	94.3	368	14	US	10-175-739-338	Sequence 338, App
38	1585.5	94.3	368	14	US	10-175-740-338	Sequence 338, App
39	1585.5	94.3	368	14	US	10-175-743-338	Sequence 338, App
40	1585.5	94.3	368	14	US	10-176-488-338	Sequence 338, App
41	1585.5	94.3	368	14	US	10-176-492-338	Sequence 338, App
42	1585.5	94.3	368	14	US	10-176-747-338	Sequence 338, App
43	1585.5	94.3	368	14	US	10-176-750-338	Sequence 338, App
44	1585.5	94.3	368	14	US	10-176-985-338	Sequence 338, App
45	1585.5	94.3	368	14	US	10-176-987-338	Sequence 338, App

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OM protein - protein search, using sw model

Run on: June 14, 2005, 16:16:02 ; Search time 39 Seconds
(without alignments)
774.668 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	541	32.2	376	2	D96550	hypothetical prote
2	510	30.3	377	2	S60478	probable 1-acyl-sn
3	496.5	29.5	374	2	S52645	probable 1-acyl-gl
4	394.5	23.5	310	2	T06755	probable glycerol-
5	389.5	23.2	311	2	T07936	probable glycerol-
6	346	20.6	393	2	B96780	hypothetical prote
7	292	17.4	350	2	T40466	probable acetyltra
8	279	16.6	397	2	S45900	probable membrane
9	221.5	13.2	396	2	S54641	probable membrane
10	215	12.8	344	2	T31913	hypothetical prote
11	208.5	12.4	918	2	T34057	hypothetical prote
12	196.5	11.7	523	2	T25998	hypothetical prote
13	191	11.4	439	2	T22689	hypothetical prote
14	170	10.1	363	2	T20608	hypothetical prote

15	161	9.6	304	2	B83541	probable polynucle
16	152	9.0	295	2	B83587	probable polynucle
17	140.5	8.4	310	2	S40808	polynucleotide ade
18	140.5	8.4	310	2	G86073	probable endonucle
19	140.5	8.4	310	2	A91227	probable endonucle
20	133	7.9	294	2	D82371	probable polynucle
21	129	7.7	391	2	T15366	hypothetical prote
22	126	7.5	279	2	T50125	probable 1-acylgly
23	126	7.5	302	2	AI0950	probable acyltrans
24	114.5	6.8	247	2	G72223	hypothetical prote
25	112	6.7	303	2	A48600	probable sn2-acylg
26	102.5	6.1	936	2	T26521	hypothetical prote
27	101.5	6.0	142	2	T29793	hypothetical prote
28	96.5	5.7	257	2	A83645	probable acyltrans
29	91.5	5.4	955	2	F84972	valine-tRNA ligase
30	88	5.2	247	2	A81957	1-acylglycerol-3-p
31	87	5.2	288	2	H95940	probable xanthine
32	86.5	5.1	301	2	E82440	hypothetical prote
33	86	5.1	247	2	G81013	1-acyl-sn-glycerol
34	86	5.1	358	2	C86291	hypothetical prote
35	86	5.1	451	2	F75131	hypothetical prote
36	86	5.1	591	2	F69837	asparagine synthet
37	86	5.1	956	2	B71250	valine-tRNA ligase
38	85.5	5.1	531	2	T11596	hypothetical prote
39	85.5	5.1	699	2	C97176	cation transport P
40	84.5	5.0	283	2	F90681	taurine dioxygenas
41	84.5	5.0	283	2	B85532	taurine dioxygenas
42	84.5	5.0	416	2	B88493	protein F57B9.5 [i
43	84	5.0	752	2	G69457	ribonucleoside-dip
44	83.5	5.0	608	2	H90530	conserved hypothet
45	83.5	5.0	1322	2	T15689	hypothetical prote

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OM protein - protein search, using sw model

Run on: June 14, 2005, 16:19:22 ; Search time 123 Seconds
(without alignments)
1307.259 Million cell updates/sec

Title: US-10-667-462-15

Perfect score: 1682

Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	1682	100.0	376	1	PLCC_HUMAN	Q9nrz7 homo sapien
2	1662	98.8	392	2	Q6ZUC6	Q6zuc6 homo sapien
3	1632	97.0	307	2	Q8N3Q7	Q8n3q7 homo sapien
4	1598	95.0	376	2	Q7TT39	Q7tt39 mus musculu
5	1598	95.0	376	2	Q9D517	Q9d517 m mus muscu
6	1589	94.5	314	2	Q8BST2	Q8bst2 mus musculu
7	1585.5	94.3	368	2	Q6UWP6	Q6uwp6 homo sapien
8	1432	85.1	376	2	Q66J57	Q66j57 xenopus lae
9	1428	84.9	376	2	Q66IJ5	Q66ij5 xenopus tro
10	1420	84.4	376	2	Q7ZYI1	Q7zyi1 xenopus lae
11	1286.5	76.5	377	2	Q7ZWC9	Q7zwc9 brachydanio
12	1138	67.7	377	2	Q6IRA0	Q6ira0 xenopus lae
13	1094	65.0	378	1	PLCD_HUMAN	Q9nrz5 h 1-acyl-sn
14	1085	64.5	378	2	Q8K4X7	Q8k4x7 m lysophosp
15	1084	64.4	377	2	Q6PGY2	Q6pgy2 brachydanio
16	1084	64.4	378	1	PLCD_RAT	Q924s1 rattus norv

17	645	38.3	386	2	Q9VV51	Q9vv51 drosophila
18	644.5	38.3	442	2	Q7QIX2	Q7qix2 anopheles g
19	622	37.0	380	2	Q9VV49	Q9vv49 drosophila
20	541	32.2	376	2	Q9SYC8	Q9syc8 arabidopsis
21	521.5	31.0	391	2	Q6IWY1	Q6iwyl brassica ol
22	517.5	30.8	390	2	Q9XFW4	Q9xfw4 brassica na
23	513.5	30.5	389	2	Q8LG50	Q8lg50 arabidopsis
24	510	30.3	377	2	Q40119	Q40119 limnanthes
25	496.5	29.5	374	2	Q41745	Q41745 zea mays (m
26	485	28.8	306	2	Q9SDN3	Q9sdn3 prunus dulc
27	394.5	23.5	310	2	Q9SVX9	Q9svx9 arabidopsis
28	392	23.3	237	2	Q7X9L2	Q7x9l2 triticum ae
29	389.5	23.2	311	2	Q39317	Q39317 brassica na
30	358	21.3	375	2	Q9LHN4	Q9lhn4 arabidopsis
31	350	20.8	378	2	Q8L4Y2	Q8l4y2 arabidopsis
32	346	20.6	373	2	Q9SSH0	Q9ssh0 arabidopsis
33	346	20.6	393	2	Q9C9P8	Q9c9p8 arabidopsis
34	292	17.4	350	2	O94361	O94361 schizosacch
35	279.5	16.6	414	2	Q6UWP7	Q6uwp7 homo sapien
36	279	16.6	397	1	YB42_YEAST	P38226 saccharomyc
37	267.5	15.9	428	2	Q7S0V1	Q7s0v1 neurospora
38	252	15.0	388	2	Q6NYV8	Q6nyv8 brachydanio
39	248.5	14.8	409	2	Q6C336	Q6c336 yarrowia li
40	243.5	14.5	411	2	Q75CU2	Q75cu2 ashbya goss
41	238.5	14.2	397	2	Q6FQP4	Q6fqp4 candida gla
42	237.5	14.1	404	2	Q6CW53	Q6cw53 kluyveromyc
43	228	13.6	356	2	Q6NUM7	Q6num7 homo sapien
44	228	13.6	364	1	PLCE_HUMAN	Q9nuq2 homo sapien
45	221.5	13.2	396	1	YD18_YEAST	Q12185 saccharomyc